AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning at page 23, line 11 with the following paragraph:

Novel genes in the sequence of clone 178D12 were predicted in silico with Genscan (24) and Fgenes software. Predicted genes were confirmed by sequencing RT-PCR products. DYXC1 cDNA has been deposited in GenBank with accession number AF337549. Mouse mDYXC1 was constructed from two overlapping EST sequences (accession numbers BG242087 and AK005832) and verified by comparing it to all available mouse mDYXC1 EST sequences. cDNA sequences of mDYXC1 and hDYXC1 were aligned with ClustalX. The alignment was improved manually, and shaded with BOXSHADE. The secondary structure of the TA rich region was predicted with MFOLD (available at http://bioinfo.math.rpi.edu/~mfold/dna/form1.cgi) with default parameters. The expression of DYXC1 was analyzed by RT-PCR from Clontech's multiple tissue cDNA panels 1 and 2. RT-PCR was performed in 25 µl volume in the following conditions: 94°C 2' (94°C 1', 68°C 2') x 30, 1 x DyNAzyme buffer with MgCl₂ (Finnzymes, Espoo, Finland), 0.2 u DyNAzyme II polymerase (Finnzymes), 15 pmol forward primer GTTGACAGAATGCTGTTCCACGTCG (SEQ ID NO:11), 15 pmol reverse primer CAAGCTGAGGCACGAAGAGCAATGA (SEQ ID NO:12). Promoter region of DYXC1 was predicted with TSSG and TSSW software at Baylor College of Medicine, available at http://searchlauncher.bem.tmc.edu/seq-search/gene-search.htmlthe Baylor College of Medicine website, and neural network promoter prediction (NNPP) software at University of California, Berkeley, available at http://www.fruitfly.org/seq-tools/promoter.htmlthe University of California, Berkeley website. The genomic sequences of nonhuman primates corresponding to

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all exons were determined by direct sequencing after PCR amplification with human-specific intronic primers (primer sequences are listed in Table 3).

Please replace the paragraph beginning at page 23, line 1 with the following paragraph:

Table 3. Human-specific intronic primers for DYXC1 (SEQ ID NOS: 22-42).

Primer		Primer			SEQ ID
Name	Primer Sequence	Length	Product Length	Exon	<u>NO:</u>
EKN1-1F	AACAGACTGCCTGGTGCTCT	20	268 bp	exon 1	<u>22</u>
EKN1-1R	CACACCAAAGTTTGAGAACCACT	23			23
EKN1-2.1R	AAGATGAGCCTGTTGCTCGT	20	476 bp	exon 2	24
EKN1-2.1F	CAAGCAGAGGGTATGGGTCTAC	22			<u>25</u>
EKN1-2R	AGAAGCTTCGGACCACACC	19	431 bp	exon 2	<u>26</u>
EKN1-3F	CGCGTGCTTAATTTGTGTAA	20	299 bp	exon 3	<u>27</u>
EKN1-3R	TCCCCTACACAATATAGGTGCTT	23			28
EKN1-4F	AAAGAAATCTCATCCTGGGTCA	22	327 bp	exon 4	<u>29</u>
EKN1-4R	GAAAATGCTGAGGAAGTCCAG	21			30
EKN1-5F	CAATGGCAAGAGTTTAGAGGTATG	24	456 bp	exon 5	31
EKN1-5R	TCAATGTGCCAAAACAGTAACC	22			32
EKN1-6F	TGTTTAGGATTTGGGGGTGA	20	395 bp	exon 6	<u>33</u>
EKN1-6R	GGAAATTCTAAAACATATTCATGACG	26			34
EKN1-7F	CCACTGGAGGAAGATGGAAA	20	244 bp	exon 7	35
EKN1-7R	TGTCTTCATACATGATAAAGCTCAT	25			<u>36</u>
EKN1-8F	GGTAAGCCATCCTCTTTGTCA	21	337 bp	exon 8	<u>37</u>
EKN1-8R	TCAACTGAACAGAAAAAGATCATCA	25			38
EKN1-9F	CTCCCCAAGTGTTGGGATTA	20	305 bp	exon 9	<u>39</u>
EKN1-9R	TGGAGTCCTTAAAAGTCACGA	21			<u>40</u>
EKN1-10F	GGTACTTGTTCTGAACCATGCTACTA	26	502 bp	exon 10	41
126403-F	CAAGGGCAAGCTTAATTCAGTAACACA	27			42